

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,767

DATE: 10/11/2001

TIME: 10:21:37

Input Set : A:\0147-0223P.ST25.txt

Output Set: N:\CRF3\10112001\I806767.raw

3 <110> APPLICANT: BERGER, Dieter et al.
 5 <120> TITLE OF INVENTION: MEANS AND METHODS FOR MODULATING STOMATA CHARACTERISTICA IN
 PLANTS

7 <130> FILE REFERENCE: 0147-0223P

9 <140> CURRENT APPLICATION NUMBER: 09/806,767

10 <141> CURRENT FILING DATE: 2001-04-03

12 <160> NUMBER OF SEQ ID NOS: 97

14 <170> SOFTWARE: PatentIn version 3.1

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 2328

18 <212> TYPE: DNA

19 <213> ORGANISM: Arabidopsis thaliana

21 <220> FEATURE:

22 <221> NAME/KEY: CDS

23 <222> LOCATION: (1)..(2325)

24 <223> OTHER INFORMATION:

27 <400> SEQUENCE: 1

ENTERED

p. 5

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32 tct tct tcg tca gag atc ctg cag aag cag act tac att gtt cag ctt	96
33 Ser Ser Ser Ser Glu Ile Leu Gln Lys Gln Thr Tyr Ile Val Gln Leu	
34 20 25 30	
36 cat cct aat agc gaa acc gct aaa acc ttt gcc tca aag ttt gat tgg	144
37 His Pro Asn Ser Glu Thr Ala Lys Thr Phe Ala Ser Lys Phe Asp Trp	
38 35 40 45	
40 cat ctt tct ttt ctc caa gaa gcg gtt tta ggt gtt gaa gaa gaa gag	192
41 His Leu Ser Phe Leu Gln Glu Ala Val Leu Gly Val Glu Glu Glu Glu	
42 50 55 60	
44 gaa gag cct tct tct cga ctt ctc tac tcc tat ggc tct gcg att gaa	240
45 Glu Glu Pro Ser Ser Arg Leu Leu Tyr Ser Tyr Gly Ser Ala Ile Glu	
46 65 70 75 80	
48 gga ttt gct gct cag ttg act gaa tca gaa gcc gag ata ctg aga tat	288
49 Gly Phe Ala Ala Gln Leu Thr Glu Ser Glu Ala Glu Ile Leu Arg Tyr	
50 85 90 95	
52 tca cct gaa gtt gtt gca gtg aga cct gac cat gtt ctt cag gtt caa	336
53 Ser Pro Glu Val Val Ala Val Arg Pro Asp His Val Leu Gln Val Gln	
54 100 105 110	
56 acc act tac tct tac aag ttc ttg gga ctc gac ggt ttt gga aac tcc	384
57 Thr Thr Tyr Ser Tyr Lys Phe Leu Gly Leu Asp Gly Phe Gly Asn Ser	
58 115 120 125	
60 ggt gta tgg tct aaa tct cgg ttt ggt caa ggc aca att atc ggc gtg	432
61 Gly Val Trp Ser Lys Ser Arg Phe Gly Gln Gly Thr Ile Ile Gly Val	
62 130 135 140	
64 ctt gat act gga gtt tgg cct gaa agt cct agc ttt gac gat acc gga	480
65 Leu Asp Thr Gly Val Trp Pro Glu Ser Pro Ser Phe Asp Asp Thr Gly	
66 145 150 155 160	
68 atg cct tcg att cca cgg aaa tgg aaa ggg att tgc caa gaa gga gaa	528

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69	Met	Pro	Ser	Ile	Pro	Arg	Lys	Trp	Lys	Gly	Ile	Cys	Gln	Glu	Gly	Glu	
70					165					170					175		
72	agt	ttc	agt	tct	tcg	agc	tgt	aac	cgg	aag	cta	atc	ggt	gct	aga	ttc	576
73	Ser	Phe	Ser	Ser	Ser	Ser	Cys	Asn	Arg	Lys	Leu	Ile	Gly	Ala	Arg	Phe	
74				180					185					190			
76	ttc	atc	aga	gga	cac	cgt	gtc	gct	aat	tca	cca	gag	gaa	tca	cca	aac	624
77	Phe	Ile	Arg	Gly	His	Arg	Val	Ala	Asn	Ser	Pro	Glu	Glu	Ser	Pro	Asn	
78			195					200					205				
80	atg	cct	cgt	gaa	tac	att	tcc	gca	aga	gat	tca	acg	gga	cac	ggg	act	672
81	Met	Pro	Arg	Glu	Tyr	Ile	Ser	Ala	Arg	Asp	Ser	Thr	Gly	His	Gly	Thr	
82		210					215					220					
84	cac	acc	gcc	tca	aca	gtt	ggt	gga	tcc	tct	gtt	tcg	atg	gcg	aat	gtt	720
85	His	Thr	Ala	Ser	Thr	Val	Gly	Gly	Ser	Ser	Val	Ser	Met	Ala	Asn	Val	
86	225				230					235					240		
88	ctt	ggc	aat	gga	gct	ggt	gtg	gct	cgt	ggg	atg	gct	cct	gga	gct	cac	768
89	Leu	Gly	Asn	Gly	Ala	Gly	Val	Ala	Arg	Gly	Met	Ala	Pro	Gly	Ala	His	
90				245					250					255			
92	att	gca	gtc	tat	aaa	gtc	tgt	tgg	ttc	aat	ggt	tgt	tac	agc	tct	gac	816
93	Ile	Ala	Val	Tyr	Lys	Val	Cys	Trp	Phe	Asn	Gly	Cys	Tyr	Ser	Ser	Asp	
94			260					265					270				
96	att	cta	gca	gct	ata	gat	gta	gcg	att	caa	gat	aaa	gtc	gat	gtt	ctt	864
97	Ile	Leu	Ala	Ala	Ile	Asp	Val	Ala	Ile	Gln	Asp	Lys	Val	Asp	Val	Leu	
98			275				280					285					
100	tcg	ctt	tcc	ctt	ggc	ggt	ttc	cct	att	cct	ttg	tat	gat	gac	aca	atc	912
101	Ser	Leu	Ser	Leu	Gly	Gly	Phe	Pro	Ile	Pro	Leu	Tyr	Asp	Asp	Thr	Ile	
102		290					295					300					
104	gcc	att	gga	aca	ttc	cga	gcc	atg	gaa	cgc	ggt	ata	tct	gta	atc	tgt	960
105	Ala	Ile	Gly	Thr	Phe	Arg	Ala	Met	Glu	Arg	Gly	Ile	Ser	Val	Ile	Cys	
106	305				310					315					320		
108	gca	gct	ggt	aac	aac	ggt	cca	atc	gaa	agc	tct	gtt	gca	aac	aca	gct	1008
109	Ala	Ala	Gly	Asn	Asn	Gly	Pro	Ile	Glu	Ser	Ser	Val	Ala	Asn	Thr	Ala	
110				325					330					335			
112	cct	tgg	gtc	tca	acc	att	ggc	gca	ggc	acg	ctt	gat	cga	aga	ttt	ccc	1056
113	Pro	Trp	Val	Ser	Thr	Ile	Gly	Ala	Gly	Thr	Leu	Asp	Arg	Arg	Phe	Pro	
114			340					345					350				
116	gct	gtg	gtc	aga	tta	gcc	aac	gga	aag	ctt	ctc	tat	gga	gag	tca	ttg	1104
117	Ala	Val	Val	Arg	Leu	Ala	Asn	Gly	Lys	Leu	Leu	Tyr	Gly	Glu	Ser	Leu	
118			355				360					365					
120	tat	ccg	gga	aaa	ggt	ata	aag	aat	gcc	ggg	aga	gag	gtt	gag	gtg	att	1152
121	Tyr	Pro	Gly	Lys	Gly	Ile	Lys	Asn	Ala	Gly	Arg	Glu	Val	Glu	Val	Ile	
122		370				375				380							
124	tac	gtc	aca	gga	gga	gat	aaa	gga	agt	gag	ttc	tgt	ttg	aga	ggg	tca	1200
125	Tyr	Val	Thr	Gly	Gly	Asp	Lys	Gly	Ser	Glu	Phe	Cys	Leu	Arg	Gly	Ser	
126	385				390					395					400		
128	ctt	cca	aga	gaa	gaa	atc	cga	ggc	aaa	atg	gtg	att	tgt	gat	cgc	gga	1248
129	Leu	Pro	Arg	Glu	Glu	Ile	Arg	Gly	Lys	Met	Val	Ile	Cys	Asp	Arg	Gly	
130				405				410					415				
132	gtc	aat	gga	aga	tcg	gag	aaa	gga	gaa	gcg	gtt	aaa	gaa	gct	gga	gga	1296
133	Val	Asn	Gly	Arg	Ser	Glu	Lys	Gly	Glu	Ala	Val	Lys	Glu	Ala	Gly	Gly	

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134	420	425	430	
136	gtt gca atg atc tta gcc aat aca gag atc aac caa gaa gaa gat tct			1344
137	Val Ala Met Ile Leu Ala Asn Thr Glu Ile Asn Gln Glu Glu Asp Ser			
138	435	440	445	
140	att gac gtt cat ctc tta cca gct aca ttg att ggt tac act gag tca			1392
141	Ile Asp Val His Leu Leu Pro Ala Thr Leu Ile Gly Tyr Thr Glu Ser			
142	450	455	460	
144	gtc ctt ctg aag gct tat gtt aat gcc acg gtg aaa cca aag gcg cgg			1440
145	Val Leu Leu Lys Ala Tyr Val Asn Ala Thr Val Lys Pro Lys Ala Arg			
146	465	470	475	480
148	ata att ttt ggt ggt acg gtg att ggg agg tca cga gca ccg gag gtg			1488
149	Ile Ile Phe Gly Gly Thr Val Ile Gly Arg Ser Arg Ala Pro Glu Val			
150	485	490	495	
152	gct cag ttt tca gct cga gga ccg agt tta gcc aat cct tcg ata cta			1536
153	Ala Gln Phe Ser Ala Arg Gly Pro Ser Leu Ala Asn Pro Ser Ile Leu			
154	500	505	510	
156	aaa ccg gat atg att gct ccg gga gtc aat atc att gcg gct tgg cct			1584
157	Lys Pro Asp Met Ile Ala Pro Gly Val Asn Ile Ile Ala Ala Trp Pro			
158	515	520	525	
160	caa aat cta gga cca acc gga ctt cct tat gat tca aga aga gtt aac			1632
161	Gln Asn Leu Gly Pro Thr Gly Leu Pro Tyr Asp Ser Arg Arg Val Asn			
162	530	535	540	
164	ttc act gta atg tca gga act tca atg tct tgt cca cat gtt agc gga			1680
165	Phe Thr Val Met Ser Gly Thr Ser Met Ser Cys Pro His Val Ser Gly			
166	545	550	555	560
168	atc act gct ctt atc cgg tct gca tac ccg aac tgg tct cca gct gca			1728
169	Ile Thr Ala Leu Ile Arg Ser Ala Tyr Pro Asn Trp Ser Pro Ala Ala			
170	565	570	575	
172	atc aaa tcc gca ttg atg aca aca gcg gat ttg tac gat cgt caa ggg			1776
173	Ile Lys Ser Ala Leu Met Thr Thr Ala Asp Leu Tyr Asp Arg Gln Gly			
174	580	585	590	
176	aaa gcg ata aag gat ggt aac aaa cca gcc ggt gtg ttt gcg att gga			1824
177	Lys Ala Ile Lys Asp Gly Asn Lys Pro Ala Gly Val Phe Ala Ile Gly			
178	595	600	605	
180	gca ggg cat gtg aat ccg caa aag gcg ata aac ccg gga ttg gtt tac			1872
181	Ala Gly His Val Asn Pro Gln Lys Ala Ile Asn Pro Gly Leu Val Tyr			
182	610	615	620	
184	aac att caa cca gtg gat tac ata act tac ctc tgc act ctt gga ttc			1920
185	Asn Ile Gln Pro Val Asp Tyr Ile Thr Tyr Leu Cys Thr Leu Gly Phe			
186	625	630	635	640
188	aca aga tca gat att tta gca atc act cat aag aac gtg agc tgc aat			1968
189	Thr Arg Ser Asp Ile Leu Ala Ile Thr His Lys Asn Val Ser Cys Asn			
190	645	650	655	
192	gga ata ttg cgg aaa aac ccg ggt ttt agt ctc aat tac ccg tcg ata			2016
193	Gly Ile Leu Arg Lys Asn Pro Gly Phe Ser Leu Asn Tyr Pro Ser Ile			
194	660	665	670	
196	gcc gtg att ttc aaa cgt ggc aag act acg gag atg atc aca agg cgt			2064
197	Ala Val Ile Phe Lys Arg Gly Lys Thr Thr Glu Met Ile Thr Arg Arg			
198	675	680	685	

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200 gtc act aac gtt ggg agt cct aac tcg ata tac tca gtg aat gtc aag      2112
201 Val Thr Asn Val Gly Ser Pro Asn Ser Ile Tyr Ser Val Asn Val Lys
202      690      695      700
204 gct cca gag ggg atc aaa gtt att gtc aat cct aag aga ctt gtg ttc      2160
205 Ala Pro Glu Gly Ile Lys Val Ile Val Asn Pro Lys Arg Leu Val Phe
206 705      710      715      720
208 aaa cac gtg gat cag acg ctg agc tat aga gta tgg ttt gta ttg aag      2208
209 Lys His Val Asp Gln Thr Leu Ser Tyr Arg Val Trp Phe Val Leu Lys
210      725      730      735
212 aag aaa aac aga gga ggg aag gtg gct agc ttt gca caa ggg cag ttg      2256
213 Lys Lys Asn Arg Gly Gly Lys Val Ala Ser Phe Ala Gln Gly Gln Leu
214      740      745      750
216 act tgg gtc aac tct cat aat ctg atg cag cga gtt aga agt cca atc      2304
217 Thr Trp Val Asn Ser His Asn Leu Met Gln Arg Val Arg Ser Pro Ile
218      755      760      765
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222      770      775
225 <210> SEQ ID NO: 2
226 <211> LENGTH: 775
227 <212> TYPE: PRT
228 <213> ORGANISM: Arabidopsis thaliana
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237      20      25      30
240 His Pro Asn Ser Glu Thr Ala Lys Thr Phe Ala Ser Lys Phe Asp Trp
241      35      40      45
244 His Leu Ser Phe Leu Gln Glu Ala Val Leu Gly Val Glu Glu Glu Glu
245      50      55      60
248 Glu Glu Pro Ser Ser Arg Leu Leu Tyr Ser Tyr Gly Ser Ala Ile Glu
249 65      70      75      80
252 Gly Phe Ala Ala Gln Leu Thr Glu Ser Glu Ala Glu Ile Leu Arg Tyr
253      85      90      95
256 Ser Pro Glu Val Val Ala Val Arg Pro Asp His Val Leu Gln Val Gln
257      100      105      110
260 Thr Thr Tyr Ser Tyr Lys Phe Leu Gly Leu Asp Gly Phe Gly Asn Ser
261      115      120      125
264 Gly Val Trp Ser Lys Ser Arg Phe Gly Gln Gly Thr Ile Ile Gly Val
265      130      135      140
268 Leu Asp Thr Gly Val Trp Pro Glu Ser Pro Ser Phe Asp Asp Thr Gly
269 145      150      155      160
272 Met Pro Ser Ile Pro Arg Lys Trp Lys Gly Ile Cys Gln Glu Gly Glu
273      165      170      175
276 Ser Phe Ser Ser Ser Ser Cys Asn Arg Lys Leu Ile Gly Ala Arg Phe
277      180      185      190
280 Phe Ile Arg Gly His Arg Val Ala Asn Ser Pro Glu Glu Ser Pro Asn
281      195      200      205

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284 Met Pro Arg Glu Tyr Ile Ser Ala Arg Asp Ser Thr Gly His Gly Thr
285      210      215      220
288 His Thr Ala Ser Thr Val Gly Gly Ser Ser Val Ser Met Ala Asn Val
289 225      230      235      240
292 Leu Gly Asn Gly Ala Gly Val Ala Arg Gly Met Ala Pro Gly Ala His
293      245      250      255
296 Ile Ala Val Tyr Lys Val Cys Trp Phe Asn Gly Cys Tyr Ser Ser Asp
297      260      265      270
300 Ile Leu Ala Ala Ile Asp Val Ala Ile Gln Asp Lys Val Asp Val Leu
301      275      280      285
304 Ser Leu Ser Leu Gly Gly Phe Pro Ile Pro Leu Tyr Asp Asp Thr Ile
305      290      295      300
308 Ala Ile Gly Thr Phe Arg Ala Met Glu Arg Gly Ile Ser Val Ile Cys
309 305      310      315      320
312 Ala Ala Gly Asn Asn Gly Pro Ile Glu Ser Ser Val Ala Asn Thr Ala
313      325      330      335
316 Pro Trp Val Ser Thr Ile Gly Ala Gly Thr Leu Asp Arg Arg Phe Pro
317      340      345      350
320 Ala Val Val Arg Leu Ala Asn Gly Lys Leu Leu Tyr Gly Glu Ser Leu
321      355      360      365
324 Tyr Pro Gly Lys Gly Ile Lys Asn Ala Gly Arg Glu Val Glu Val Ile
325      370      375      380
328 Tyr Val Thr Gly Gly Asp Lys Gly Ser Glu Phe Cys Leu Arg Gly Ser
329 385      390      395      400
332 Leu Pro Arg Glu Glu Ile Arg Gly Lys Met Val Ile Cys Asp Arg Gly
333      405      410      415
336 Val Asn Gly Arg Ser Glu Lys Gly Glu Ala Val Lys Glu Ala Gly Gly
337      420      425      430
340 Val Ala Met Ile Leu Ala Asn Thr Glu Ile Asn Gln Glu Glu Asp Ser
341      435      440      445
344 Ile Asp Val His Leu Leu Pro Ala Thr Leu Ile Gly Tyr Thr Glu Ser
345      450      455      460
348 Val Leu Leu Lys Ala Tyr Val Asn Ala Thr Val Lys Pro Lys Ala Arg
349 465      470      475      480
352 Ile Ile Phe Gly Gly Thr Val Ile Gly Arg Ser Arg Ala Pro Glu Val
353      485      490      495
356 Ala Gln Phe Ser Ala Arg Gly Pro Ser Leu Ala Asn Pro Ser Ile Leu
357      500      505      510
360 Lys Pro Asp Met Ile Ala Pro Gly Val Asn Ile Ile Ala Ala Trp Pro
361      515      520      525
364 Gln Asn Leu Gly Pro Thr Gly Leu Pro Tyr Asp Ser Arg Arg Val Asn
365      530      535      540
368 Phe Thr Val Met Ser Gly Thr Ser Met Ser Cys Pro His Val Ser Gly
369 545      550      555      560
372 Ile Thr Ala Leu Ile Arg Ser Ala Tyr Pro Asn Trp Ser Pro Ala Ala
373      565      570      575
376 Ile Lys Ser Ala Leu Met Thr Thr Ala Asp Leu Tyr Asp Arg Gln Gly
377      580      585      590
380 Lys Ala Ile Lys Asp Gly Asn Lys Pro Ala Gly Val Phe Ala Ile Gly

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VERIFICATION SUMMARY

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L:968 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:969 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1454 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1674 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
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L:2044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:2259 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:3099 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:3103 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70
L:3249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79
L:3253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:79
L:3368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:88
L:3514 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:97